

D0047 NP

FIG. 1

ATGACGTCCACCTGCACCAACAGCACGCGGAGAGTAACAGCAGCCACACGTGCATGCCC
CTCTCCAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGGTTATC
TTCTCGCCGCCTCTTTCTGTCGGCAACATAGTGCTGGCGCTAGTGTTGCAGCGCAAGCCG
CAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAACCTCCTCGTCACCGACCTGCTGCAG
ATTTCTGCTCGTGGCCCCCTGGGTGGTGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAAC
AGCCACTTCTGCACGGCCCTGGTTAGCCTCACCCACCTGTTTCGCCTTCGCCAGCGTCAAC
ACCATTGTCTTGGTGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCTACCCG
TCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACCTGGATTGTGGCCATC
CTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCAGGCTGCCTTTGATGAGCGCAATGCT
CTCTGCTCCATGATCTGGGGGGCCAGCCCCAGCTACACTATTCTCAGCGTGGTGTCTTC
ATCGTCATTCCACTGATTGTGATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCG
AGGCAGCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCGAGTCAAGGAC
TGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAGTTCAGGATGAGAGT
GAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGCCAAGGAGGGCAGAATGGAAGCCAAG
GACGGCAGCCTGAAGGCCAAGGAAGGAAGCACGGGGACCAGTGAGAGTAGTGTAGAGGCC
AGGGGCAGCGAGGAGGTGAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGT
AAGGAAGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCACAGAG
GTCAACCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTTGGTGAAGACGACATC
AATTTCACTGAGGATGACGTCGAGGCAGTGAACATCCCGGAGAGCCTCCCACCCAGTCGT
CGTAACAGCAACAGCAACCCTCCTCTGCCCAGGTGCTACCAAGTGCAAAGCTGCTAAAGTG
ATCTTCATCATCATTTTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTTAGCAGTC
CTGGCCGTGTGGGTGGATGTGAAACCCAGGTACCCAGTGGGTGATCACCATAATCATC
TGGCTTTTCTTCTGTCAGTGTGTCATCCACCCCTATGTCTATGGCTACATGCACAAGACC
ATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTTCTTCTGCAAGGAAAAGCCCCGAAA
GAAGATAGCCACCCAGACCTGCCCCGAACAGAGGTGGGACTGAAGGCAAGATTGTCCCT
TCCTACGATTCTGCTACTTTTCCTTGA

FIG. 1

D0047 NP

FIG.2

MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
QLLQVTNRFI FNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
TIVLVSVDRLYSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWWQAADFERN
LCSMIWGASPSYTI LSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
CVENEDEEGA EKKEEFQDESEFRQHEGEVKAKEGRMEAKDGSLKAKEGSTGTSESSVEA
RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
NFSEDDVEAVNIPESLPFSRRNSNSNPPLPRCYQCKAAKVIFIIIFS YVLSLGPYCFLAV
LAVWVDVETQVPQWVITIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKKPPK
EDSHPDLPGTEGGTEGKIVPSYDSATFP

FIG. 3

GCAACCTGTCTCACGCCCTCTGGCTGTTGCC

1000 900 800 700 600 500 400 300 200 100 0

D0047 NP

FIG. 4

AGTTAGTTCTAAGGCAAACCTT

FIG. 5

1	MTSTCTNSTR	ESNSSHTCMP	LSKMPISLAH	GIIRSTVLVI	<u>FLAASFVGNI</u>
51	<u>VLALVLQRKP</u>	QLLQVTNRFI	<u>FNLLVTDLLQ</u>	<u>ISLVAPWVVA</u>	<u>TSVPLEFWPLN</u>
101	<u>SHFCTALVSL</u>	<u>THLFAFASVN</u>	<u>TIVLVSVDRY</u>	LSIIHPLSYP	SKMTQRRGYL
151	<u>LLYGTWIVAI</u>	<u>LQSTPPLYGW</u>	GQAAFDERNA	LCSMIWGASP	SYTILSVVSF
201	<u>IVIPLIVMIA</u>	<u>CYSVVFCAAR</u>	RQHALLYNVK	RHSLEVRVKD	CVENEDEEGA
251	EKKEEFQDES	EFRRQHEGEV	KAKEGRMEAK	DGSLKAKEGS	TGTSESSVEA
301	RGSEEVRESS	TVASDGSMEG	KEGSTKVEEN	SMKADKGRTE	VNQCSIDLGE
351	DDMEFGEDDI	NFSEDDVEAV	NIPESLPPSR	RNSNSNPPLP	RCYQCKAAKV
401	<u>IFIIIFSIVL</u>	<u>SLGPYCFLAV</u>	LAVWVDVETQ	VPQWVITIII	<u>WLFFLQCCIH</u>
451	<u>PYVYGYMHKT</u>	IKKEIQDMLK	KFFCKEKPPK	EDSHPDLPGT	EGGTEGKIVP
501	SYDSATFP				

D0047 NP

FIG. 6A

ACM4_CHICK	~~~~~
YDBM_CAEEL	~~~~~
5H1A_HUMAN	~~~~~
5H1A_MOUSE	~~~~~
5H1A_FUGRU	~~~~~
5HT_LYMST	~MANFTFGDLALDVARMGGLASTPSGLRSTGLTTPGLSPT
A1AD_HUMAN	MTFRDLLSVSFEGPRPDSSAGGSSAGGGGGSAGGAAPSEG
A1AD_MOUSE	MTFRDILSVTFEGPRASSSTGGSGAGGGAGTVG...P.EG
Q13675	~~~~~
Q13729	~~~~~
O60451	~~~~~
A1AA_RAT	~~~~~
O54913	~~~~~
A1AA_BOVIN	~~~~~
A1AA_CANFA	~~~~~
A1AA_RABIT	~~~~~
A1AA_HUMAN	~~~~~
A1AA_ORYLA	~~~~~
O96716	~~~~~
O75963	~~~~~
HGPRBMY8	~~~~~
ACM4_CHICK	~~~~~MHNLSAQPWQAKMANITYDNVTLSN
YDBM_CAEEL	MCFAEKGEAGEDVDHHSLFC.P.KKLVGNL...KGFIRN
5H1A_HUMAN	~~~~~MDV..LSPGQ...GNNTT...SPPAPFETGGN
5H1A_MOUSE	~~~~~MDM..FSLGQ...GNNTT...TSLEPFGTGGN
5H1A_FUGRU	~~~~~MDLRATSSND...SNATSGYSDTAAWDWDEGEN
5HT_LYMST	GLVTSDFNDSYGLT.GQFINGSHSSRSRDNASANDTSATN
A1AD_HUMAN	PAVGGVPGGAGGGGGVVGAGSGEDNRSSAGEPGSAGAGGD
A1AD_MOUSE	PAVGGVP.GATGGSVVGTGSGEDNQSSTAEGAA.ASGE
Q13675	~~~~~MVFLSGNASDS
Q13729	~~~~~MVFLSGNASDS
O60451	~~~~~MVFLSGNASDS
A1AA_RAT	~~~~~MVLLSENASEG
O54913	~~~~~MVLLSENASEG
A1AA_BOVIN	~~~~~MVFLSGNASDS
A1AA_CANFA	~~~~~MVFLSGNASDS
A1AA_RABIT	~~~~~MVFLSGNASDS
A1AA_HUMAN	~~~~~MVFLSGNASDS
A1AA_ORYLA	~~~~~MTPSSVTLNC
O96716	~~~~~MSANTTVSPTETTANLTANSTEA
O75963	~~~~~MSLNSSL
HGPRBMY8	~~~~~MTSTCTNSTRESNS

D0047 NP

FIG. 6B

ACM4_CHICK	RSEVAIQPPTNYKTVELVFIATVTGSL..LVTVVGNILV
YDBM_CAEEL	QYH.....QHETIQ.ILKGSALFLV..LWTIFANSLV
5H1A_HUMAN	ITG...ISDVTVSYQ..VITSLLLGTLI..FCAVLGNACV
5H1A_MOUSE	DTG...LSNVTFYSYQ..VITSLLLGTLI..FCAVLGNACV
5H1A_FUGRU	ATGSGSLPDPELSYQ..IITSIFLGALI..LCSTFGNSCV
5HT_LYMST	MTDDRYWSLTVYSHEHLVLTSVILGLFV..LCCIIGNCFV
A1AD_HUMAN	V.NGTAAVGGLVVSQAQGVGVFLAAFI..LMAVAGNLLV
A1AD_MOUSE	V.NGSAAVGGLVVSQAQGVGVFLAAFI..LTAVAGNLLV
Q13675	S.NCTQPPAP.VNISKAILLGVLGGLI..LFCVLGNILV
Q13729	S.NCTQPPAP.VNISKAILLGVLGGLI..LFCVLGNILV
O60451	S.NCTQPPAP.VNISKAILLGVLGGLI..LFCVLGNILV
A1AA_RAT	S.NCTHPPAP.VNISKAILLGVLGGLI..IFCVLGNILV
O54913	S.NCTHPPAQ.VNISKAILLGVLGGLI..IFCVLGNILV
A1AA_BOVIN	S.NCTHPPP.VNISKAILLGVLGGLI..LFCVLGNILV
A1AA_CANFA	S.NCTHPPAP.VNISKAILLGVLGGLI..IFCVLGNILV
A1AA_RABIT	S.NCTHPPAP.VNISKAILLGVLGGLI..LFCVLGNILV
A1AA_HUMAN	S.NCTQPPAP.VNISKAILLGVLGGLI..LFCVLGNILV
A1AA_ORYLA	S.NCSHVLAPEINTVKAIVLGMVLGIFI..LFCVLGNILV
O96716	SVGSCFAPNPYSAGVQAV.LGLITVILI..LLTVIGNVLV
O75963	CRKELSNLTEEEGGEGGVITQFIATIVITIEVCLGNLVI
HGPRBMY8	SHTCMPLSKMPTSLAHGIIIRSTVL..VIFLAASFVGNIVL
ACM4_CHICK	MLSIKVNRLQQTVNNYFLFSLACADLIIGVFSMNLYTVYI
YDBM_CAEEL	FIVLYKNPRLQQTVPNLLVGNLAFSDLATGLIVLPLSSVYA
5H1A_HUMAN	VAAIALERSLQNVANYLIGSLAVTDLMVSVLVLPMAALYQ
5H1A_MOUSE	VAAIALERSLQNVANYLIGSLAVTDLMVSVLVLPMAALYQ
5H1A_FUGRU	VAAIALERSLQNVANYLIGSLAVTDLMVSVLVLPMAALYQ
5HT_LYMST	IAAVMLERSLHNVANLYLISLAVADLMVAVLVMPLSVVSE
A1AD_HUMAN	IILSVACNRHLQQTVTNYEIVNLAVADLLLSTVLPFSATME
A1AD_MOUSE	IILSVACNRHLQQTVTNYEIVNLAVADLLLSTVLPFSATME
Q13675	IILSVACHRHLHSVTHYYIVNLAVADLLLSTVLPFSATFE
Q13729	IILSVACHRHLHSVTHYYIVNLAVADLLLSTVLPFSATFE
O60451	IILSVACHRHLHSVTHYYIVNLAVADLLLSTVLPFSATFE
A1AA_RAT	IILSVACHRHLHSVTHYYIVNLAVADLLLSTVLPFSATFE
O54913	IILSVACHRHLHSVTHYYIVNLAVADLLLSTVLPFSATFE
A1AA_BOVIN	IILSVACHRHLHSVTHYYIVNLAVADLLLSTVLPFSATFE
A1AA_CANFA	IILSVACHRHLHSVTHYYIVNLAVADLLLSTVLPFSATFE
A1AA_RABIT	IILSVACHRHLHSVTHYYIVNLAVADLLLSTVLPFSATFE
A1AA_HUMAN	IILSVACHRHLHSVTHYYIVNLAVADLLLSTVLPFSATFE
A1AA_ORYLA	IILSVVCHRHLQQTVTYYEIVNLAVADLLLSTVLPFSATFE
O96716	ILAVTCHRMRTVTNREIVSLACADLSVGITVLPFAATND
O75963	VVTLYKKSyllLTLNKTVFSLTLSNfLLSVLVLPFVVTSS
HGPRBMY8	ALVLQRPQLLOVTNREIFNLLVTDLLQISLVAPWVATS

D0047 NP

FIG. 6C

ACM4_CHICK	IKGYWPLGAVVCDIWLALDYVVSNASVMNLLIISFDRYFC
YDBM_CAEL	IAGEWVFPDALCEVFSADILCSTASIWNLSTVGLDRYWA
5H1A_HUMAN	VLNKWTLGQVTCDFIALDVLCCCTSSILHLCAIALDRYWA
5H1A_MOUSE	VLNKWTLGQVTCDFIALDVLCCCTSSILHLCAIALDRYWA
5H1A_FUGRU	VLNKWTLGQDICDFIALDVLCCCTSSILHLCAIALDRYWA
5HT_LYMST	ISKVWFLHSEVCDMWISVDVLCCTASILHLVAIAMDRYWA
A1AD_HUMAN	VLGEWAFGRAFCDVWAAVDVLCCTASILSLCTISVDRYVG
A1AD_MOUSE	VLGEWPFGRTECDVWAAVDVLCCTASILSLCTISVDRYVG
Q13675	VLGYWAFGRVFCNIWAAVDVLCCTASIMGLCTISIDRYIG
Q13729	VLGYWAFGRVFCNIWAAVDVLCCTASIMGLCTISIDRYIG
O60451	VLGYWAFGRVFCNIWAAVDVLCCTASIMGLCTISIDRYIG
A1AA_RAT	ILGYWAFGRVFCNIWAAVDVLCCTASIMGLCTISIDRYIG
O54913	ILGYWAFGRVFCNIWAAVDVLCCTASIMGLCTISIDRYIG
A1AA_BOVIN	ILGYWAFGRVFCNVWAAVDVLCCTASIMGLCTISIDRYIG
A1AA_CANFA	ILGYWAFGRVFCNIWAAVDVLCCTASIMGLCTISIDRYIG
A1AA_RABIT	ILGYWAFGRVFCNIWAAVDVLCCTASILSLCVISIDRYIG
A1AA_HUMAN	VLGYWAFGRVFCNIWAAVDVLCCTASIMGLCTISIDRYIG
A1AA_ORYLA	ILDRWVFGRVFCNIWAAVDVLCCTASIMSLCVISVDRYIG
O96716	ILGYWPFGG.YCDVWVSFDVLNSTASILNLVVIAFDRELA
O75963	IRREWIFGVVWCNFSALLYLLISSASMLTLGVIAIDRYYA
HGPRBMY8	VPLEWPLNSHFCTALVSLTHLFAFASVNTIVLVSVDRYLS
ACM4_CHICK	VTKPLTYPARRTTKMAGLMIAAAWILSFLIWPAT.LFW.
YDBM_CAEL	ITSPVAYMSKRNRKTAGTMIISVWISSALISLAPL.LGWK
5H1A_HUMAN	ITDPIDYVNKRTPRRAAALISLTWLGFLISIPPM.LGW.
5H1A_MOUSE	ITDPIDYVNKRTPRRAAALISLTWLGFLISIPPM.LGW.
5H1A_FUGRU	ITDPIDYVNKRTPRRAAVLISVTWLGFSISIPPM.LGW.
5HT_LYMST	VTS.IDYIRRRSARRILMIMVWVIVALFISIPPL.FGW.
A1AD_HUMAN	VRHSLKYPAIMTERKAAAILALLWVVALVSVVGPL.LGW.
A1AD_MOUSE	VRHSLKYPAIMTERKAAAILALLWVVALVSVVGPL.LGW.
Q13675	VSYPTRYPTIVTQRRGLMALLCVWALSLVISIGPL.FGW.
Q13729	VSYPTRYPTIVTQRRGLMALLCVWALSLVISIGPL.FGW.
O60451	VSYPTRYPTIVTQRRGLMALLCVWALSLVISIGPL.FGW.
A1AA_RAT	VSYPTRYPTIVTQRRGVRALLCVWVLSLVISIGPL.FGW.
O54913	VSYPTRYPTIVTQRRGVRALLCVWALSLVISIGPL.FGW.
A1AA_BOVIN	VSYPTRYPTIVTQKRLMALLCVWALSLVISIGPL.FGW.
A1AA_CANFA	VSYPTRYPTIVTQKRLMALLCVWALSLVISIGPL.FGW.
A1AA_RABIT	VSYPTRYPTIVTQRRGLRALLCVWAFSLVISVGPL.FGW.
A1AA_HUMAN	VSYPTRYPTIVTQRRGLMALLCVWALSLVISIGPL.FGW.
A1AA_ORYLA	VSYPTRYPAIMTKRRALLAVMLLWVLSVVISIGPL.FGW.
O96716	ITAPFTYHTRMTERTAGILIAIVWGISLVVSFLPIQAGWY
O75963	VLYPMVYPMKITGNRAVMALVYIWLHSLIGCLPPL.FGWS
HGPRBMY8	LIHPLSYPSKMTORRGYLLYGTWIVALLQSTPPL.YGWG

D0047 NP

FIG. 6D

ACM4_CHICK	QFIVGKRTVHE.....RECYIQFLSNPAVTFGTATAAFYL
YDBM_CAEEL	QTAQTPLNIYEKNNTVRQC..TFLDLPSYTVYSATGSEFI
5H1A_HUMAN	R.TP.EDRSDPDA.....CTIS..KDHGYTIYSTFGAFYL
5H1A_MOUSE	R.AP.EDRSNPNE.....CTIS..KDHGYTIYSTFGAFYL
5H1A_FUGRU	R.SA.EDRANPDA.....CIIS..QDPGYTIYSTFGAFYL
5HT_LYMST	R.DENNDPDKTGT.....CIIS..QDKGYTIYSTFGAFYL
A1AD_HUMAN	K.EPVPP.....DERFCGIT..EEAGYAVFSSVCSFYI
A1AD_MOUSE	K.EPVPP.....DERFCGIT..EEVGYAIFSSVCSFYI
Q13675	R.QPAPE.....DETICQIN..EEPGYVLFSALGSFYI
Q13729	R.QPAPE.....DETICQIN..EEPGYVLFSALGSFYI
O60451	R.QPAPE.....DETICQIN..EEPGYVLFSALGSFYI
A1AA_RAT	R.QPAPE.....DETICQIN..EEPGYVLFSALGSFYV
O54913	R.QQAPE.....DETICQIN..EEPGYVLFSALGSFYV
A1AA_BOVIN	R.QPAPE.....DETICQIN..EEPGYVLFSALGSFYV
A1AA_CANFA	R.QPAPE.....DETICQIT..EEPGYVLFSALGSFYV
A1AA_RABIT	R.QPAPD.....DETICQIN..EEPGYVLFSALGSFYV
A1AA_HUMAN	R.QPAPE.....DETICQIN..EEPGYVLFSALGSFYI
A1AA_ORYLA	K.EPAPE.....DETVCKIT..EEPGYAIFSAVGSFYI
O96716	R.DNQSEELAIYS DPCLCIFT..ASTAYTIVSSLSFYI
O75963	S.VEFDEFKWM.....CVAAWH..REPGYTAFWQIWCALE
HGPRBMY8	QA.....AFDERNALCSMIWGASPSYTIILSVVSFIV
ACM4_CHICK	PVVIMTVLYIHISLA.SRSRVRRHKPESRKERKKGKSLSFF
YDBM_CAEEL	PTLIMFFVYFKIYQAFAKHRARQIYRQKVIRKHIESTILH
5H1A_HUMAN	PLLLMLVLYGRIFRA.....ARFRIRKTVKKVEK.....
5H1A_MOUSE	PLLLMLVLYGRIFRA.....ARFRIRKTVKKVEK.....
5H1A_FUGRU	PLILMLVLYGRIFKA.....ARFRIRKTVKKTEKA.....
5HT_LYMST	PMLVMMIYYIRIWL.....ARSRIKDKFQMTKARL...
A1AD_HUMAN	PMAVIVVMYCRVYVV.....A.....RSTTRSL...
A1AD_MOUSE	PMAVIVVMYCRVYVV.....A.....RSTTRSL...
Q13675	PLAIILVMYCRVYVV.....A.....KRESRGL...
Q13729	PLAIILVMYCRVYVV.....A.....KRESRGL...
O60451	PLAIILVMYCRVYVV.....A.....KRESRGL...
A1AA_RAT	PLAIILVMYCRVYVV.....A.....KRESRGL...
O54913	PLTIILVMYCRVYVV.....A.....KRESRGL...
A1AA_BOVIN	PLTIILVMYCRVYVV.....A.....KRESRGL...
A1AA_CANFA	PLTIILVMYCRVYVV.....A.....KRESRGL...
A1AA_RABIT	PLTIILVMYCRVYVV.....A.....KRESRGL...
A1AA_HUMAN	PLAIILVMYCRVYVV.....A.....KRESRGL...
A1AA_ORYLA	PLAIILVMYCRVYVV.....A.....QKESRGL...
O96716	PLILMLVLYFYGIIFKA.....A.....PDQARKI...
O75963	PFLVMLVCYGFIFRV.....ARV.....KARKV...
HGPRBMY8	PLIVMTIACYSVVFCARRQHA.LLYNVKRHSLEVRVKDCV

D0047 NP

FIG. 6E

ACM4_CHICK	KAPPVKQNNNN	SPKRAVEVKEEVRNGKVDDQPSAQTEATG
YDBM_CAEEL	EISHVLPTSDEFAKEEEEEEDSESSGQVENGL	CNGNDAI.
5H1A_HUMANTGADTRHGASPAQPK..KSVNG....E..	
5H1A_MOUSEKGAGTSFGTSSAPPPK..KSLNG....Q..	
5H1A_FUGRUKASDMCLTLSPAVFHK..RA.NG....D..	
5HT_LYMSTKTEETTLVASPKTEYSVSDCNCNSPD..	
A1AD_HUMANEA.....	GVKRER..
A1AD_MOUSEEA.....	GIKREP..
Q13675KS.....	GLKTDK..
Q13729KS.....	GLKTDK..
O60451KS.....	GLKTDK..
A1AA_RATKS.....	GLKTDK..
O54913KS.....	GLKTDK..
A1AA_BOVINKS.....	GLKTDK..
A1AA_CANFAKS.....	GLKTDK..
A1AA_RABITKS.....	GLKTDK..
A1AA_HUMANKS.....	GLKTDK..
A1AA_ORYLAKE.....	GOKIEK..
O96716NA.....	LEG....
O75963HCGTVVIVEEDAQRTGRKNSSTSTSSSG..	
HGPRBMY8	ENEDEEGAEEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDG	
ACM4_CHICK	QQEEKETSNESSTVSMTQTTKDKPTTEILPAGQGQSPAHP	
YDBM_CAEEL	.IEEDECEDEDSDEKRDHITS...MTTVTATVTGPTEA.P	
5H1A_HUMAN	..SGSRNWRLGVESKAGGALCANGAVRQDDGAAL.EVIE	
5H1A_MOUSE	..PGSGDCRRSAENRAVGTPCANGAVRQGEDDATL.EVIE	
5H1A_FUGRU	..AVSAEWKRGYKFKP..SSPCANGAVRHGEEMESL.EVIE	
5HT_LYMST	..STTEKKKRRAPFKSYG..CSPRPERKKNRAKKLPENAN	
A1AD_HUMAN	..GKAS.....	EVVL
A1AD_MOUSE	..GKAS.....	EVVL
Q13675	..SDSE.....	QVTL
Q13729	..SDSE.....	QVTL
O60451	..SDSE.....	QVTL
A1AA_RAT	..SDSE.....	QVTL
O54913	..SDSE.....	QVTL
A1AA_BOVIN	..SDSE.....	QVTL
A1AA_CANFA	..SDSE.....	QVTL
A1AA_RABIT	..SDSE.....	QVTL
A1AA_HUMAN	..SDSE.....	QVTL
A1AA_ORYLA	..SDSE.....	QVIL
O96716	
O75963	..SRNAFQGVVYSANQCKALITILVVLGAFMVTWGPYM	
HGPRBMY8	SLKAKEGSTGTSESSVEARGSEEVRESSTVASDGSMEGKE	

D0047 NP

FIG. 6F

ACM4_CHICK	RVNPTSKWSKIKIVTKQTGTESVTAIEIVPAKAGASDHNS
YDBM_CAEEL	YMKREAKISKSVPIEKESAIQKREAKPMRSVMAISYEKVK
5H1A_HUMAN	.VHRVGNSKEHLPL....PSEAGPT....PCAP....ASF
5H1A_MOUSE	.VHRVGNSKGDPL....PSESGAT....SYVP....ACL
5H1A_FUGRU	.VN..SNSKTHLPL....PN....T....P.QS....SSH
5HT_LYMST	GVNSNSSSSERLKQIQIETAEAFAN....GCAEEASTAML
A1AD_HUMAN	RIHC.....RGAAT....GADGAHGMRSA
A1AD_MOUSE	RIHC.....RGAAT....SAKGNPGTQSS
Q13675	RIHR.....KNAPA.....GGSGMASA
Q13729	RIHR.....KNAPA.....GGSGMASA
O60451	RIHR.....KNAPA.....GGSGMASA
A1AA_RAT	RIHR.....KNVPA.....EGGGVSSA
O54913	RIHR.....KNVPA.....EGSGVSSA
A1AA_BOVIN	RIHR.....KNAQV.....GGSGVTSA
A1AA_CANFA	RIHR.....KNAPV.....GGTGVSSA
A1AA_RABIT	RIHR.....KNAPA.....GGSGVASA
A1AA_HUMAN	RIHR.....KNAPA.....GGSGMASA
A1AA_ORYLA	RMHR.....GNTTV.....SEDEAL
O96716	RLEQ.....EN.....NRGKKISLA
O75963	VI...ASEALWGKSSVSPSLETWAT...WLSFASAVCHP
HGPRBMY8	GSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDINF

ACM4_CHICK	LSNSRPANVARKFASLARSQVRKKRQMAAR..EKKVTRTI
YDBM_CAEEL	RHKNRKERIYRK..SLQR...KPKAISAAK..ERRGVKVL
5H1A_HUMAN	ERK..NERN.....AEAKRKMA..LAR..ERKTVKTL
5H1A_MOUSE	ERK..NERT.....AEAKRKMA..LAR..ERKTVKTL
5H1A_FUGRU	ENI..NEKT.....TGTRRKLA..LAR..ERKTVKTL
5HT_LYMST	ERQCNGGKKISSNDTPYSRTREKLE..LKR..ERKAAKTL
A1AD_HUMAN	KG.....HTFRSSLV.....RLLK..FSR..EKKAATL
A1AD_MOUSE	KG.....HTLRSSLV.....RLLK..FSR..EKKAATL
Q13675	KT.....KT...HFSV.....RLLK..FSR..EKKAATL
Q13729	KT.....KT...HFSV.....RLLK..FSR..EKKAATL
O60451	KT.....KT...HFSV.....RLLK..FSR..EKKAATL
A1AA_RAT	KN.....KT...HFSV.....RLLK..FSR..EKKAATL
O54913	KN.....KT...HFSV.....RLLK..FSR..EKKAATL
A1AA_BOVIN	KN.....KT...HFSV.....RLLK..FSR..EKKAATL
A1AA_CANFA	KN.....KT...HFSV.....RLLK..FSR..EKKAATL
A1AA_RABIT	KN.....KT...HFSV.....RLLK..FSR..EKKAATL
A1AA_HUMAN	KT.....KT...HFSV.....RLLK..FSR..EKKAATL
A1AA_ORYLA	RS.....RT...HFAT.....RLLK..FSR..EKKAATL
O96716	K.....EKKAATL
O75963	LIYGLWNKTIVRKELLMCFGRYYEPEFVQ..RQTSRLF
HGPRBMY8	SEDDVEAVNIPESLPPSRNSNS.NPPLPRCYQCKAAKV

D0047 NP

FIG. 6G

ACM4_CHICK FAIILAFILITWTPYNVMVLINTFC..ETCVPET.VWSIGY
YDBM_CAEEL GIILGCFTVCWAPFFETMYVLVQFC..KDCSPNAHIEMFIT
5H1A_HUMAN GIIMGTFILCWLPPFFIVALVLPF.CESSCHMPTLLGAIN
5H1A_MOUSE GIIMGTFILCWLPPFFIVALVLPF.CESSCHMPELLGAIN
5H1A_FUGRU GIIMGTFILCWLPPFFIVALVLPF.CAENCYMPEWLGAVIN
5HT_LYMST AIIITGAFLICWLPPFFITALIGPF.VDPE.GIPPFARSEVL
A1AD_HUMAN AIVVGVEVLCWEPFFFEVLPLGSL.F.POLKPSSEGVFKVIF
A1AD_MOUSE AIVVGVEVLCWEPFFFEVLPLGSL.F.POLKPSSEGVFKVIF
Q13675 GIVVGCFLCWLPPFFVMPIGSF.F.PDFKPSSETVFKIVF
Q13729 GIVVGCFLCWLPPFFVMPIGSF.F.PDFKPSSETVFKIVF
O60451 GIVVGCFLCWLPPFFVMPIGSF.F.PDFKPSSETVFKIVF
A1AA_RAT GIVVGCFLCWLPPFFVMPIGSF.F.PDFKPSSETVFKIVF
O54913 GIVVGCFLCWLPPFFVMPIGSF.F.PDFKPSSETVFKIVF
A1AA_BOVIN GIVVGCFLCWLPPFFVMPIGSF.F.PDFKPSSETVFKIVF
A1AA_CANFA GIVVGCFLCWLPPFFVMPIGSF.F.PDFKPSSETVFKIVF
A1AA_RABIT GIVVGCFLCWLPPFFVMPIGSF.F.PDFKPSSETVFKIVF
A1AA_HUMAN GIVVGCFLCWLPPFFVMPIGSF.F.PDFKPSSETVFKIVF
A1AA_ORYLA GIVVGCFLCWLPPFFVMPIGSF.F.PDFKPSSETVFKIVF
O96716 GIIMGVFILCWLPPF.VVNIIVNP.F.CDRCVQPAVFIALT
O75963 SISNRITDLGLSPHLTALMAGGQPLGHSSSTGDTGFSCSQ
HGPRBMY8 FIIIFSVLSLGPYCFIAVL.AVWVDVETQVPQWVITII

ACM4_CHICK WLCYVNSTINPACYALCNATFKKTFKHLMCQYRNIGTAR
YDBM_CAEEL WLGYSNSAMNPIIYTVFNRDYQIALKRIETSEKKPSSTSR
5H1A_HUMAN WLGYSNSLLNPIIYAYFNKDFQNAFKKIKCKFCRQ~~~~
5H1A_MOUSE WLGYSNSLLNPIIYAYFNKDFQNAFKKIKCKFCR~~~~
5H1A_FUGRU WLGYSNSLLNPIIYAYFNKDFQSAFKKILRCKFHRH~~~~
5HT_LYMST WLGYFNSLLNPIIYTIYSPEFRSAFQKILFGKYRRGHR~~~
A1AD_HUMAN WLGYFNSCVNPIIYPCSSREFKRAFLRLRLC.QCRRRRR.
A1AD_MOUSE WLGYFNSCVNPIIYPCSSREFKRAFLRLRLC.QCRRRRR.
Q13675 WLGYLNSCINPIIYPCSSQEFKKAQONVLR.I.QCLRKKQS
Q13729 WLGYLNSCINPIIYPCSSQEFKKAQONVLR.I.QCLRKKQS
O60451 WLGYLNSCINPIIYPCSSQEFKKAQONVLR.I.QCLRKKQS
A1AA_RAT WLGYLNSCINPIIYPCSSQEFKKAQONVLR.I.QCLRKKQS
O54913 WLGYLNSCINPIIYPCSSQEFKKAQONVLR.I.QCLRKKQS
A1AA_BOVIN WLGYLNSCINPIIYPCSSQEFKKAQONVLR.I.QCLRKKQS
A1AA_CANFA ~~~~~~
A1AA_RABIT WLGYLNSCINPIIYPCSSQEFKKAQONVLR.I.QCLRKKQS
A1AA_HUMAN WLGYLNSCINPIIYPCSSQEFKKAQONVLR.I.QCLRKKQS
A1AA_ORYLA WLGYFNSCINPIIYLCSNQEFKKAQONVLR.I.QCLRKKQS
O96716 WLGYFNSCINPIIYAFNKEFRKVFKMICCHKCRGVTVG
O75963 DSGNLRAL~~~~~
HGPRBMY8 WLFELQCCIHFYVGYMHKTIKKEIQDMLKKFFCKEKKPPK

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FIG. 6H

```
ACM4_CHICK ~~~~~
YDBM_CAEEL V~~~~~
5H1A_HUMAN ~~~~~
5H1A_MOUSE ~~~~~
5H1A_FUGRU ~~~~~
5HT_LYMST ~~~~~
A1AD_HUMAN .RRPLWRVY..GHHWRASTSGTRQDCAPSSGDAPPGAPLA
A1AD_MOUSE .R..LW.....PSLRPPLASL..DRRPALRLCPQPAHRT
Q13675 SKH...ALG..YT.LHPPSQAVEGQHKDM.VRIPVGSRET
Q13729 SKH...ALG..YT.LHPPSQAVEGQHKDM.VRIPVGSRET
O60451 SKH...ALG..YT.LHPPSQAVEGQHKDM.VRIPVGSRET
A1AA_RAT SKH...ALG..YT.LHPPSQALEGQHRDM.VRIPVGSGET
O54913 SKH...ALG..YT.LHPPSQAVEEQHRGM.VRIPVGSGET
A1AA_BOVIN SKH...TLG..YT.LHAPSHVLEGQHKDL.VRIPVGSGET
A1AA_CANFA ~~~~~
A1AA_RABIT SKH...ALG..YT.LHAPSQALEGQHKDM.VRIPVGSGET
A1AA_HUMAN SKH...ALG..YT.LHPPSQAVEGQHKDM.VRIPVGSRET
A1AA_ORYLA AHHHHLSVG..QSQTQGHSLTISLDSKGAPCRLSPSSSVA
O96716 PNHADLNYDPVAMRLKKRGENANGTVNGDANGKANGNIEA
O75963 ~~~~~
HGPRBMY8 ED SHPDLPGTEGGTEGKIVPSYDSATFP~~~~~

ACM4_CHICK ~~~~~
YDBM_CAEEL ~~~~~
5H1A_HUMAN ~~~~~
5H1A_MOUSE ~~~~~
5H1A_FUGRU ~~~~~
5HT_LYMST ~~~~~
A1AD_HUMAN LTALPDPD..PEP...PGTPEMQAPVASRRKPPSA...FR
A1AD_MOUSE PRGSPSPH..CTPR..PGLRRHAGGAGFGLRPSKASLRLR
Q13675 FYRISKTDGVCEWKFFSSMPRG SARITVSKDQSSCTTART
Q13729 FYRISKTDGVCEWKFFSSMPRG SARITVSKDQSSCTTARG
O60451 FYRISKTDGVCEWKFFSSMPRG SARITVSKDQSSCTTARR
A1AA_RAT FYKISKTDGVCEWKFFSSMPQGSARITV PKDQSACTTARV
O54913 FYKISKTDGVCEWKFFSSMPQGSARITM PKDQSACTTARV
A1AA_BOVIN FYKISKTDGVCEWKIFSSLPRGSARMAVARDPSACTTARV
A1AA_CANFA ~~~~~
A1AA_RABIT FYKISKTDGVCEWKFFSSMPRG SARITV PKDQSACTTARV
A1AA_HUMAN FYRISKTDGVCEWKFFSSMPRG SARITVSKDQSSCTTARV
A1AA_ORYLA LSRT PSSRDSREWRVFSGGPINSGL..PGPTEAGRAKVAKL
O96716 GEGTSSS~~~~~
O75963 ~~~~~
HGPRBMY8 ~~~~~
```

D0047 NP

FIG. 6I

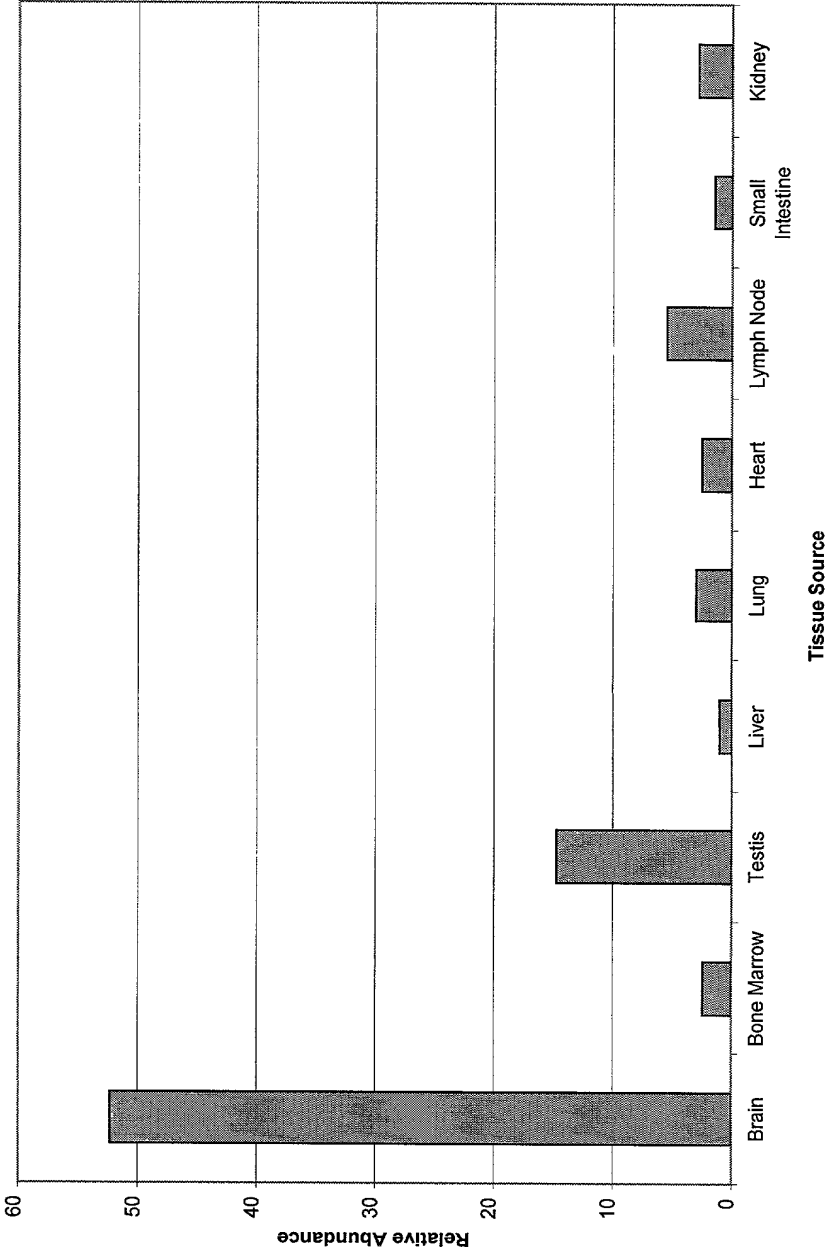
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5H1A_MOUSE	~~~~~
5H1A_FUGRU	~~~~~
5HT_LYMST	~~~~~
A1AD_HUMAN	EWRLLGPFRRPTTQLRAKVSSSLSHKIRAGGAQRAEAACAQ
A1AD_MOUSE	EWRLLGPLQRPTTQLRAKVSSSLSHKFRSGGARRAETACAL
Q13675	KRSVTRLECS...GMILAHCN..LRLPGSRDSPASASQ
Q13729	HT.PMT~~~~~
O60451	GMDCRYFTKNC...REHIKHVN..FMMPPWRKGLEC~~~
A1AA_RAT	RSKSFLQVCCCV.GSSAPRPEEN..HQVPTIKIHTISLGE
O54913	RSKSFLQVCCCV.GSSTPRPEEN..HQVPTIKIHTISLGE
A1AA_BOVIN	RSKSFLQVCCCL.GPSTPSHGEN..HQIPTIKIHTISLSE
A1AA_CANFA	~~~~~
A1AA_RABIT	RSKSFLQVCCCV.GPSTPNPGEN..HQVPTIKIHTISLSE
A1AA_HUMAN	RSKSFLQVCCCV.GPSTPSLDKN..HQVPTIKVHTISLSE
A1AA_ORYLA	CNKSLHRTCCCILRARTPTQDPAPLGDLPTIKIHQLSLSE
O96716	~~~~~
O75963	~~~~~
HGPRBMY8	~~~~~
ACM4_CHICK	~~~~~
YDBM_CAEEL	~~~~~
5H1A_HUMAN	~~~~~
5H1A_MOUSE	~~~~~
5H1A_FUGRU	~~~~~
5HT_LYMST	~~~~~
A1AD_HUMAN	RSEVEAVSLGVPHEVAEGATCQAYELADYSNLRETDI~~~
A1AD_MOUSE	RSEVEAVSLNVPQDGAEAVICQAYEPGDLSNLRETDI~~~
Q13675	AAGTTGDVPPGRRHQAQLIFVFLVETGFHHVGQDDLDLLT
Q13729	~~~~~
O60451	~~~~~
A1AA_RAT	NGEEV~~~~~
O54913	NGEEV~~~~~
A1AA_BOVIN	NGEEV~~~~~
A1AA_CANFA	~~~~~
A1AA_RABIT	NGEEV~~~~~
A1AA_HUMAN	NGEEV~~~~~
A1AA_ORYLA	KGESV~~~~~
O96716	~~~~~
O75963	~~~~~
HGPRBMY8	~~~~~

D0047 NP

FIG. 6J

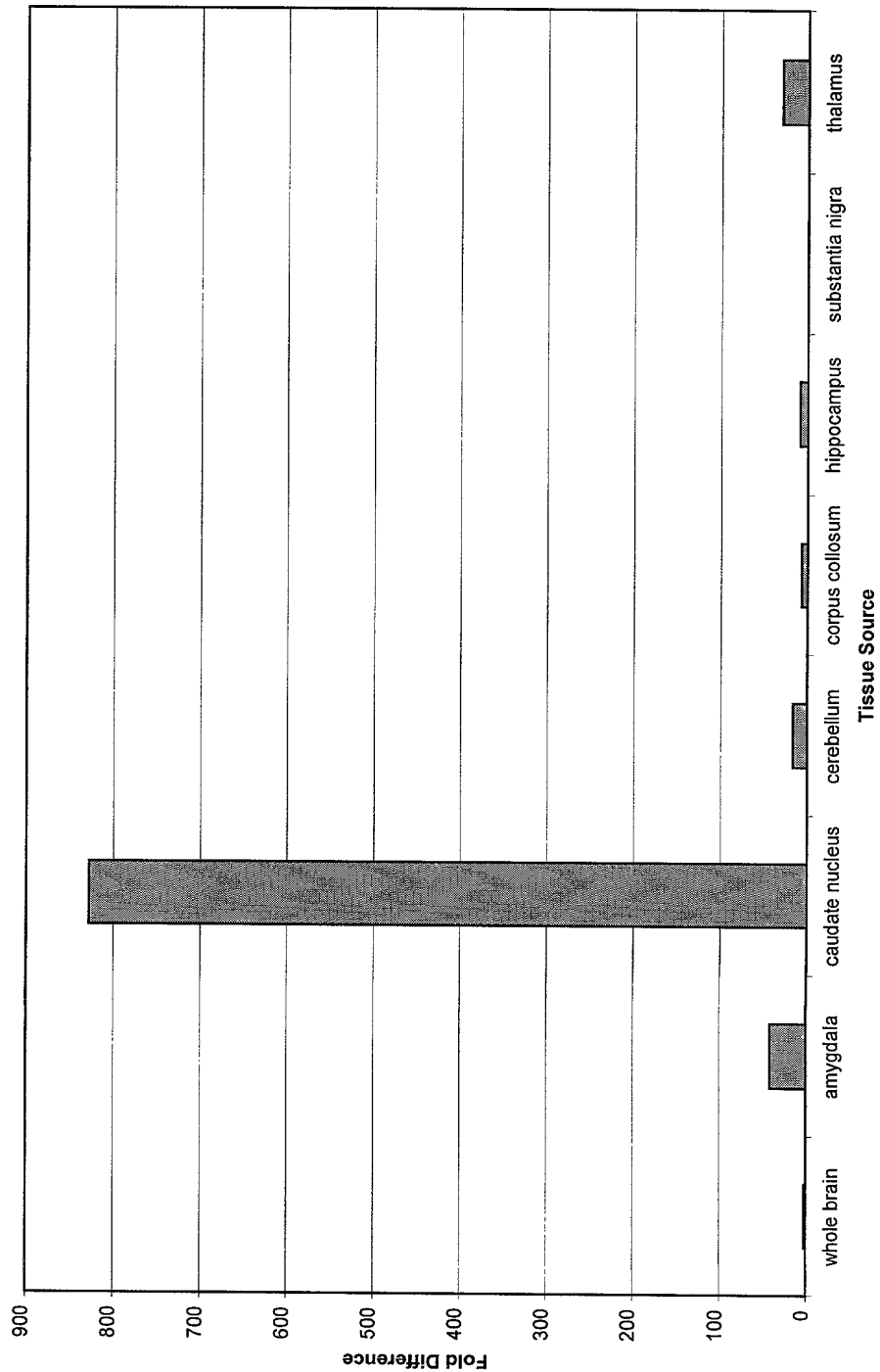
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YDBM_CAEEL	~
5H1A_HUMAN	~
5H1A_MOUSE	~
5H1A_FUGRU	~
5HT_LYMST	~
A1AD_HUMAN	~
A1AD_MOUSE	~
Q13675	S
Q13729	~
O60451	~
A1AA_RAT	~
O54913	~
A1AA_BOVIN	~
A1AA_CANFA	~
A1AA_RABIT	~
A1AA_HUMAN	~
A1AA_ORYLA	~
O96716	~
O75963	~
HGPRBMY8	~

FIG. 7



D0047 NP

FIG. 8



D0047 NP

FIG. 9

HGPRBMY8 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
AL390879 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
AX148250 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
AX080495 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP

HGPRBMY8 QLLQVTNRFI FNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
AL390879 QLLQVTNRFI FNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
AX148250 QLLQVTNRFI FNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
AX080495 QLLQVTNRFI FNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN

HGPRBMY8 TIVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA
AL390879 TIVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA
AX148250 TIVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA
AX080495 TIVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA

HGPRBMY8 LCSMIWGASPSYITILSVVSFIVIPLIACYSVVFCARRQHALLYNVKRHSLEVRVKD
AL390879 LCSMIWGASPSYITILSVVSFIVIPLIACYSVVFCARRQHALLYNVKRHSLEVRVKD
AX148250 LCSMIWGASPSYITILSVVSFIVIPLIACYSVVFCARRQHALLYNVKRHSLEVRVKD
AX080495 LCSMIWGASPSYITILSVVSFIVIPLIACYSVVFCARRQHALLYNVKRHSLEVRVKD

HGPRBMY8 CVENEDEEGAEEKKEEFQDESEFRQHEGEVKAKEGRMEAKDGLKAKEGSTGTSESSVEA
AL390879 CVENEDEEGAEEKKEEFQDESEFRQHEGEVKAKEGRMEAKDGLKAKEGSTGTSESSVEA
AX148250 CVENEDEEGAEEKKEEFQDESEFRQHEGEVKAKEGRMEAKDGLKAKEGSTGTSESSVEA
AX080495 CVENEDEEGAEEKKEEFQDESEFRQHEGEVKAKEGRMEAKDGLKAKEGSTGTSESSVEA

HGPRBMY8 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
AL390879 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
AX148250 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
AX080495 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI

HGPRBMY8 NFEEDDVEAVNIPESLPPSRNRNSNSNPPLPRCYQCKAAKVIFIIIFSIVLSLGPYCFLAV
AL390879 NFEEDDVEAVNIPESLPPSRNRNSNSNPPLPRCYQCKAAKVIFIIIFSIVLSLGPYCFLAV
AX148250 NFEEDDVEAVNIPESLPPSRNRNSNSNPPLPRCYQCKAAKVIFIIIFSIVLSLGPYCFLAV
AX080495 NFEEDDVEAVNIPESLPPSRNRNSNSNPPLPRCYQCKAAKVIFIIIFSIVLSLGPYCFLAV

HGPRBMY8 LAVWVDVETQVPQWVITIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCCKEPPK
AL390879 LAVWVDVETQVPQWVITIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCCKEPPK
AX148250 LAVWVDVETQVPQWVITIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCCKEPPK
AX080495 LAVWVDVETQVPQWVITIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCCKEPPK

HGPRBMY8 EDSHPDLPGTEGGTEGKIVPSYDSATFP~
AL390879 EDSHPDLPGTEGGTEGKIVPSYDSATFP*
AX148250 EDSHPDLPGTEGGTEGKIVPSYDSATFP*
AX080495 EDSHPDLPGTEGGTEGKIVPSYDSATFP*

D0047 NP

FIG. 10A

AX080495 GCCTGCAACCTGTCTCACGCCCTCTGGCTGTTGCCATGACGTCCACCTGC
HGPRBMY8 ~~~~GCAACCTGTCTCACGCCCTCTGGCTGTTGCCATGACGTCCACCTGC
AL390879 ~~~~~~ATGACGTCCACCTGC
AX148250 ~~~~~~ATGACGTCCACCTGC

AX080495 ACCAACAGCACGCGGAGAGTAACAGCAGCCACACGTGCATGCCCCCTCTC
HGPRBMY8 ACCAACAGCACGCGGAGAGTAACAGCAGCCACACGTGCATGCCCCCTCTC
AL390879 ACCAACAGCACGCGGAGAGTAACAGCAGCCACACGTGCATGCCCCCTCTC
AX148250 ACCAACAGCACGCGGAGAGTAACAGCAGCCACACGTGCATGCCCCCTCTC

AX080495 CAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGG
HGPRBMY8 CAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGG
AL390879 CAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGG
AX148250 CAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGG

AX080495 TTATCTTCCTCGCCGCCTCTTTCGTGCGCAACATAGTGCTGGCGCTAGTG
HGPRBMY8 TTATCTTCCTCGCCGCCTCTTTCGTGCGCAACATAGTGCTGGCGCTAGTG
AL390879 TTATCTTCCTCGCCGCCTCTTTCGTGCGCAACATAGTGCTGGCGCTAGTG
AX148250 TTATCTTCCTCGCCGCCTCTTTCGTGCGCAACATAGTGCTGGCGCTAGTG

AX080495 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA
HGPRBMY8 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA
AL390879 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA
AX148250 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA

AX080495 CCTCCTCGTCACCGACCTGCTGCAGATTTGCTCGTGGCCCCCTGGGTGG
HGPRBMY8 CCTCCTCGTCACCGACCTGCTGCAGATTTGCTCGTGGCCCCCTGGGTGG
AL390879 CCTCCTCGTCACCGACCTGCTGCAGATTTGCTCGTGGCCCCCTGGGTGG
AX148250 CCTCCTCGTCACCGACCTGCTGCAGATTTGCTCGTGGCCCCCTGGGTGG

AX080495 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAACAGCCACTTCTGCACG
HGPRBMY8 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAACAGCCACTTCTGCACG
AL390879 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAACAGCCACTTCTGCACG
AX148250 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAACAGCCACTTCTGCACG

AX080495 GCCCTGGTTAGCCTCACCACCTGTTTCGCCTTCGCCAGCGTCAACACCAT
HGPRBMY8 GCCCTGGTTAGCCTCACCACCTGTTTCGCCTTCGCCAGCGTCAACACCAT
AL390879 GCCCTGGTTAGCCTCACCACCTGTTTCGCCTTCGCCAGCGTCAACACCAT
AX148250 GCCCTGGTTAGCCTCACCACCTGTTTCGCCTTCGCCAGCGTCAACACCAT

AX080495 TGTCTTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT
HGPRBMY8 TGTCTTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT
AL390879 TGTCTTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT
AX148250 TGTCTTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT

AX080495 ACCCGTCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACC
HGPRBMY8 ACCCGTCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACC
AL390879 ACCCGTCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACC
AX148250 ACCCGTCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACC

D0047 NP

FIG. 10B

AX080495	TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
HGPRBMY8	TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
AL390879	TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
AX148250	TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
AX080495	GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
HGPRBMY8	GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
AL390879	GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
AX148250	GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
AX080495	GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
HGPRBMY8	GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
AL390879	GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
AX148250	GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
AX080495	ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGGAGGCA
HGPRBMY8	ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGGAGGCA
AL390879	ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGGAGGCA
AX148250	ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGGAGGCA
AX080495	GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGAAGTGCGAGTCA
HGPRBMY8	GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGAAGTGCGAGTCA
AL390879	GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGAAGTGCGAGTCA
AX148250	GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGAAGTGCGAGTCA
AX080495	AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
HGPRBMY8	AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
AL390879	AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
AX148250	AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
AX080495	TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
HGPRBMY8	TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
AL390879	TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
AX148250	TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
AX080495	CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
HGPRBMY8	CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
AL390879	CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
AX148250	CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
AX080495	GAAGCACGGGGACCAGTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
HGPRBMY8	GAAGCACGGGGACCAGTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
AL390879	GAAGCACGGGGACCAGTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
AX148250	GAAGCACGGGGACCAGTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
AX080495	GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA
HGPRBMY8	GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA
AL390879	GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA
AX148250	GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA

D0047 NP

FIG. 10C

AX080495 AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
HGPRBMY8 AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
AL390879 AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
AX148250 AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA

AX080495 CAGAGGTCAACCAAGTGCAGCATTGACTTGGGTGAAGATGCATGGAGTTT
HGPRBMY8 CAGAGGTCAACCAAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT
AL390879 CAGAGGTCAACCAAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT
AX148250 CAGAGGTCAACCAAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT

AX080495 GGTGAAGACGACATCAATTTCACTGAGGATGACGTCGAGGCAGTGAACAT
HGPRBMY8 GGTGAAGACGACATCAATTTCACTGAGGATGACGTCGAGGCAGTGAACAT
AL390879 GGTGAAGACGACATCAATTTCACTGAGGATGACGTCGAGGCAGTGAACAT
AX148250 GGTGAAGACGACATCAATTTCACTGAGGATGACGTCGAGGCAGTGAACAT

AX080495 CCCGGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCCTCCTC
HGPRBMY8 CCCGGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCCTCCTC
AL390879 CCCGGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCCTCCTC
AX148250 CCCGGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCCTCCTC

AX080495 TGCCCAGGTGCTACCAAGTGCAGGCTGCTAAAGTGATCTTCATCATCATT
HGPRBMY8 TGCCCAGGTGCTACCAAGTGCAGGCTGCTAAAGTGATCTTCATCATCATT
AL390879 TGCCCAGGTGCTACCAAGTGCAGGCTGCTAAAGTGATCTTCATCATCATT
AX148250 TGCCCAGGTGCTACCAAGTGCAGGCTGCTAAAGTGATCTTCATCATCATT

AX080495 TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTTAGCAGTCCTGGC
HGPRBMY8 TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTTAGCAGTCCTGGC
AL390879 TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTTAGCAGTCCTGGC
AX148250 TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTTAGCAGTCCTGGC

AX080495 CGTGTGGGTGGATGTCGAAACCCAGGTACCCAGTGGGTGATCACCATAA
HGPRBMY8 CGTGTGGGTGGATGTCGAAACCCAGGTACCCAGTGGGTGATCACCATAA
AL390879 CGTGTGGGTGGATGTCGAAACCCAGGTACCCAGTGGGTGATCACCATAA
AX148250 CGTGTGGGTGGATGTCGAAACCCAGGTACCCAGTGGGTGATCACCATAA

AX080495 TCATCTGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
HGPRBMY8 TCATCTGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
AL390879 TCATCTGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
AX148250 TCATCTGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC

AX080495 TACATGCACAAGACCATTAAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
HGPRBMY8 TACATGCACAAGACCATTAAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
AL390879 TACATGCACAAGACCATTAAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
AX148250 TACATGCACAAGACCATTAAAGAAGGAAATCCAGGACATGCTGAAGAAGTT

AX080495 CTTCTGCAAGGAAAAGCCCCGAAAGAAGATAGCCACCCAGACCTGCCCG
HGPRBMY8 CTTCTGCAAGGAAAAGCCCCGAAAGAAGATAGCCACCCAGACCTGCCCG
AL390879 CTTCTGCAAGGAAAAGCCCCGAAAGAAGATAGCCACCCAGACCTGCCCG
AX148250 CTTCTGCAAGGAAAAGCCCCGAAAGAAGATAGCCACCCAGACCTGCCCG

D0047 NP

FIG. 10D

AX080495	GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCTTCCTACGATTCTGCT
HGPRBMY8	GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCTTCCTACGATTCTGCT
AL390879	GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCTTCCTACGATTCTGCT
AX148250	GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCTTCCTACGATTCTGCT

AX080495	ACTTTTCCTTGAAGTTAGTTCTAAGGCAAACCTTGAAAATCAGTCCTTCA
HGPRBMY8	ACTTTTCCTTGAAGTTAGTTCTAAGGCAAACCTT~~~~~
AL390879	ACTTTTCCTTGA~~~~~
AX148250	ACTTTTCCTTGA~~~~~

AX080495	GCCACAGCTATTTAGAGCTTTAAACTACCAGGTTCAATCACTGGTTATG
HGPRBMY8	~~~~~
AL390879	~~~~~
AX148250	~~~~~

AX080495	CTTTCTGTG
HGPRBMY8	~~~~~
AL390879	~~~~~
AX148250	~~~~~

FIG. 11

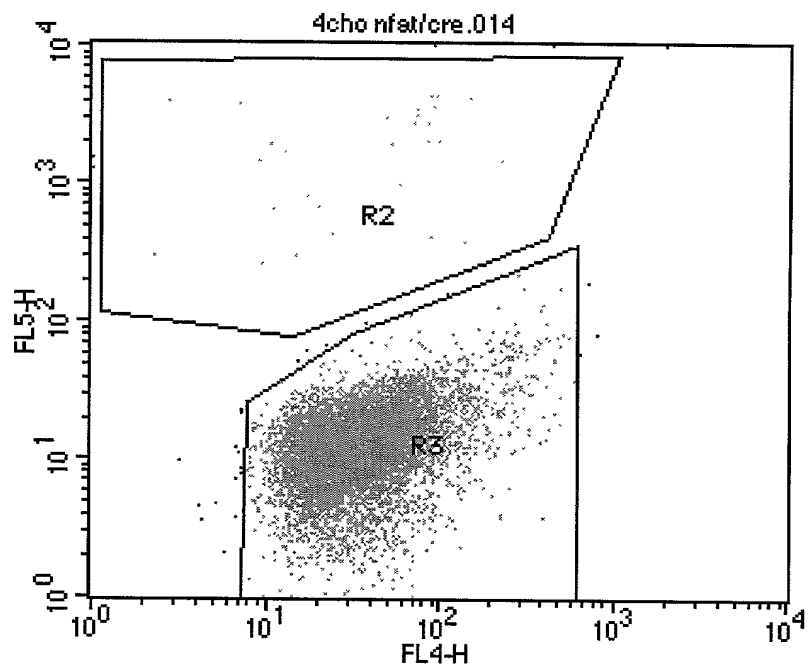


FIG. 12

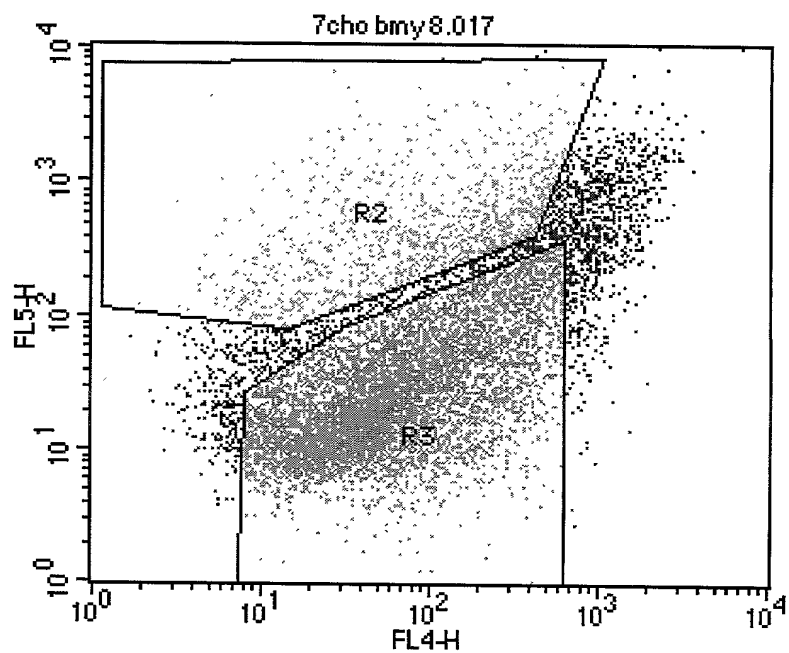


FIG. 13

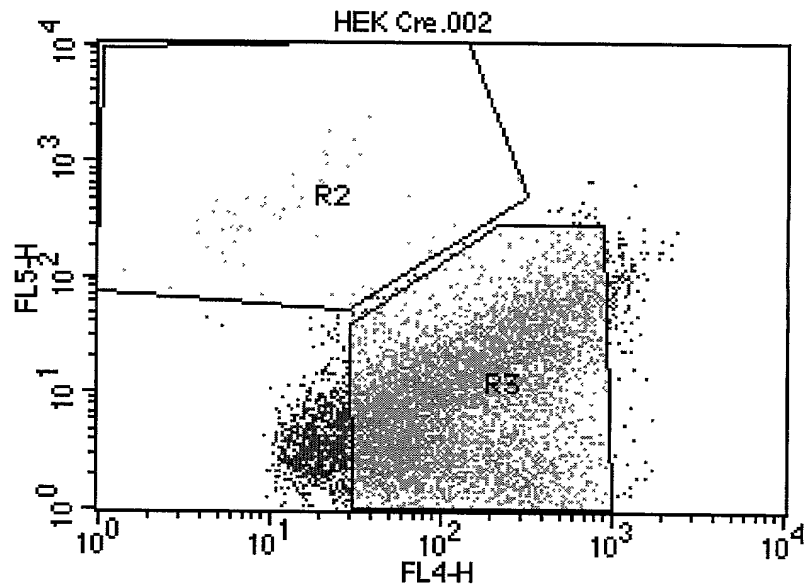
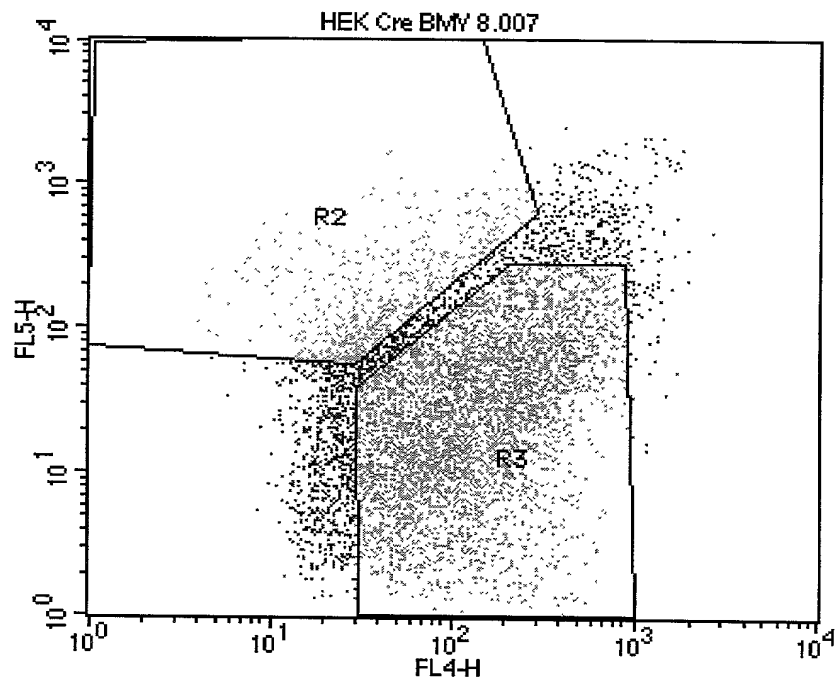


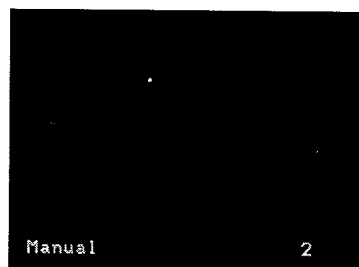
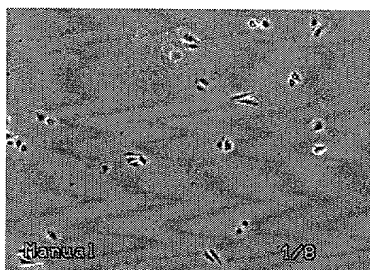
FIG. 14



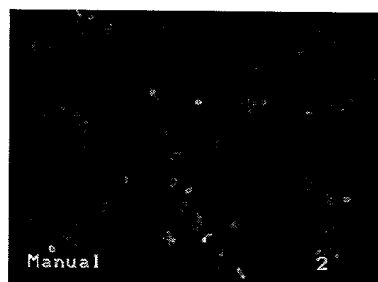
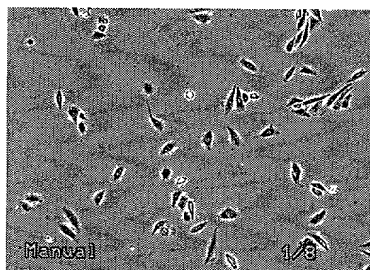
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FIG. 15

a. CHO-NFAT G alpha 15 (Fluorescent vs. Bright Field)



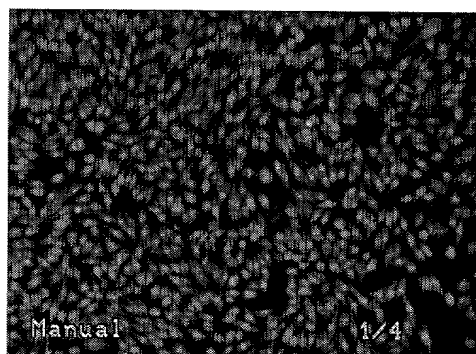
b. CHO-NFAT/ G alpha 15 HGPRBMY8 (Fluorescent vs. Bright Field)



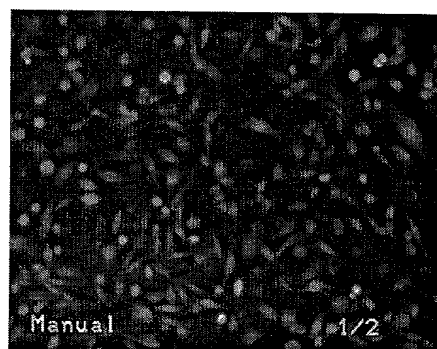
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FIG. 16

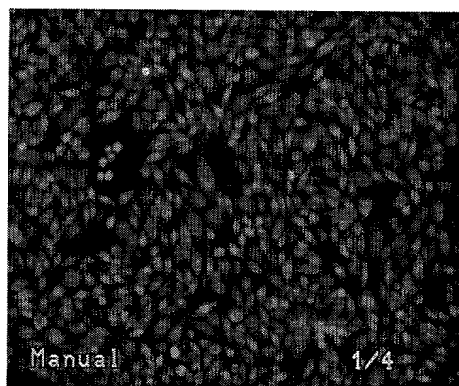
a. CHO-NFAT/CRE



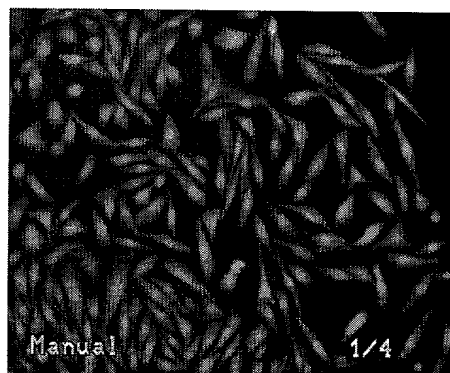
b. CHO-NFAT/CRE + F/T/P



c. CHO-NFAT/CRE oGPCR-Intermediate

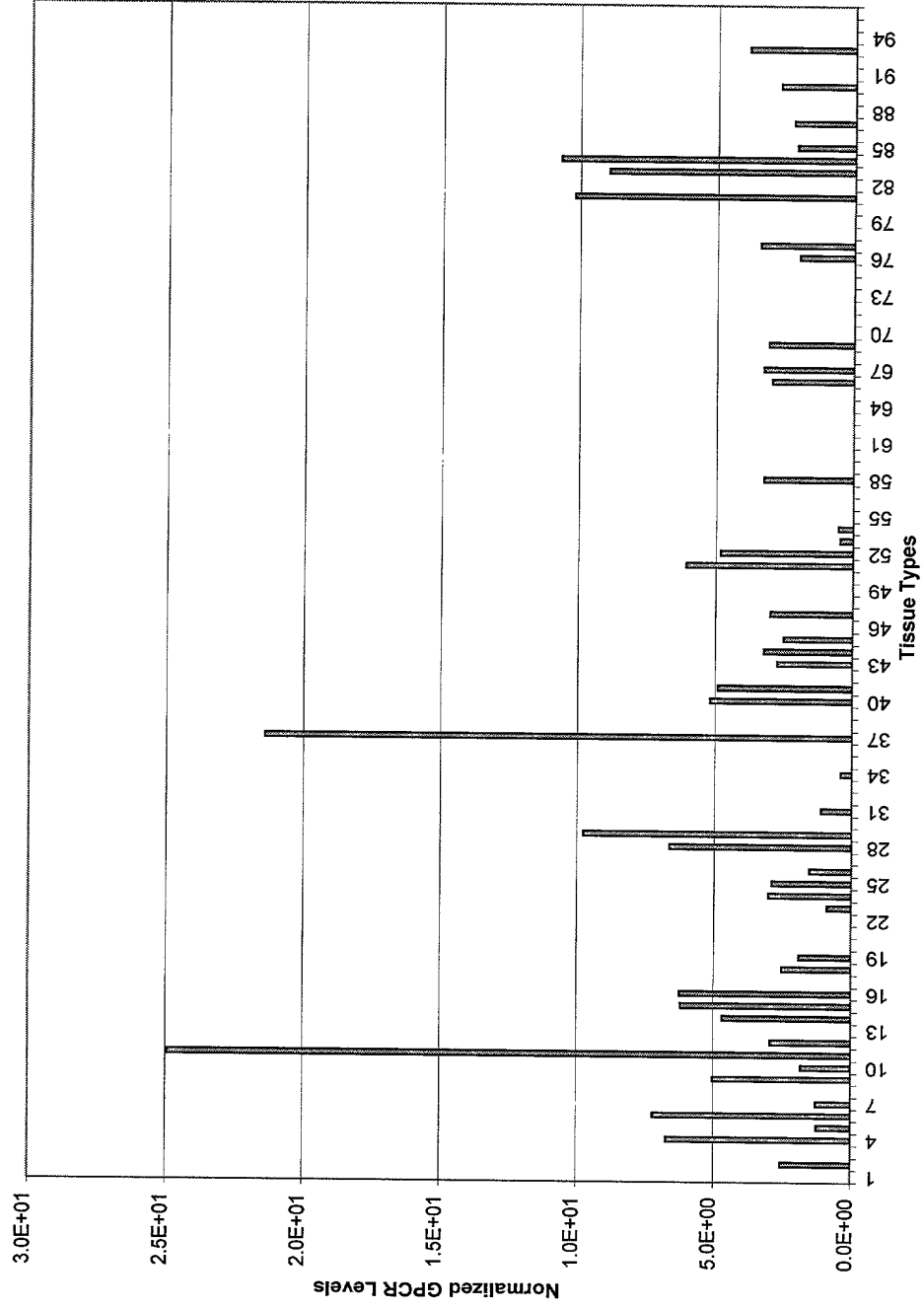


d. CHO-NFAT/CRE oGPCR high



D0047 NP

FIG. 17



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FIG. 18A

1	ATGACGTCCACCTGCACCAACAGCACGCGCGAGAGTAACAGCAGCCACACGTGCATGCCC	60
1	M T S T C T N S T R E S N S S H T C M P	20
61	CTCTCCAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGGTTATC	120
21	L S K M P I S L A H G I I R S T V L V I	40
121	TTCCTCGCCGCTCTTTCGTCGGCAACATAGTGCTGGCGCTAGTGTGTCAGCGCAAGCCG	180
41	F L A A S F V G N I V L A L V L Q R K P	60
181	CAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAACCTCCTCGTCACCGACCTGCTGCAG	240
61	Q L L Q V T N R F I F N L L V T D L L Q	80
241	ATTCGCTCGTGGCCCCCTGGGTGGTGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAAC	300
81	I S L V A P W V V A T S V P L F W P L N	100
301	AGCCACTTCTGCACGGCCCTGGTTAGCCTCACCCACCTGTTGCCTTCGCCAGCGTCAAC	360
101	S H F C T A L V S L T H L F A F A S V N	120
361	ACCATTGTCTNTGGTGTCACTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCTACCCG	420
121	T I V <u>X</u> V S V D R Y L S I I H P L S Y P	140
421	TCCAAGATGACCCAGCGCCGCGTTACCTGCTCCTCTATGGCACCTGGATTGTGGCCATC	480
141	S K M T Q R R G Y L L L Y G T W I V A I	160
481	CTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCAGGCTGCCTTTGATGAGCGCAATGCT	540
161	L Q S T P P L Y G W G Q A A F D E R N A	180
541	CTCTGCTCCATGATCTGGGGGGCCAGCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCT	600
181	L C S M I W G A S P S Y T I L S V V S F	200
601	ATCGTCATTCCACTGATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGG	660
201	I V I P L I V M I A C Y S V V F C A A R	220
661	AGGCAGCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGAAGTGCGAGTCAAGGAC	720
221	R Q H A L L Y N V K R H S L E V R V K D	240
721	TGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAGTTCAGGATGAGAGT	780
241	C V E N E D E E G A E K K E E F Q D E S	260
781	GAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGCCAAGGAGGGCAGAATGGAAGCCAAG	840
261	E F R R Q H E G E V K A K E G R M E A K	280
841	GACGGCAGCCTGAAGGCCAAGGAAGGAAGCACGGGGACCAAGTGAGAGTAGTGTAGAGGCC	900
281	D G S L K A K E G S T G T S E S S V E A	300

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FIG. 18B

901 AGGGGCAGCGAGGAGGTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGT 960
301 R G S E E V R E S S T V A S D G S M E G 320

961 AAGGAAGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCACAGAG 1020
321 K E G S T K V E E N S M K A D K G R T E 340

1021 GTCAACCAGTGCAGCATTGACTTGGGTGAAGATGNCATGGAGTTTGGTGAAGACGACATC 1080
341 V N Q C S I D L G E D X M E F G E D D I 360

1081 AATTTTCAGTGAGGATGACGTCGAGGCAGTGAACATCCCGGAGAGCCTCCACCCAGTCGT 1140
361 N F S E D D V E A V N I P E S L P P S R 380

1141 CGTAACAGCAACAGCAACCCTCCTCTGCCAGGTGCTACCAAGTCAAAGCTNNNAAAGTG 1200
381 R N S N S N P P L P R C Y Q C K A X K V 400

1201 ATCTTCATCATCATTTTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTAGCAGTC 1260
401 I F I I I F S Y V L S L G P Y C F L A V 420

1261 CTGGCCGTGTGGGTGGATGTGAAACCCAGGTACCCCAAGTGGGTGATCACCATAATCATC 1320
421 L A V W V D V E T Q V P Q W V I T I I I 440

1321 TGGCTTTTCTCCTGCAGTGTGCATCCACCCCTATGTCTATGGCTACATGCACAAGACC 1380
441 W L F F L Q C C I H P Y V Y G Y M H K T 460

1381 ATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTTCTTCTGCAAGGAAAAGCCCCGAAA 1440
461 I K K E I Q D M L K K F F C K E K P P K 480

1441 GAAGATAGCCACCCAGACCTGCCCGAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCT 1500
481 E D S H P D L P G T E G G T E G K I V P 500

1501 TCCTACGATTCTGCTACTTTTCCTTGA 1527
501 S Y D S A T F P 508

FIG. 18B